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Evaluation of identity-by-descent probabilities for half-sibs on continuous genome. (English)

Zbl 1070.92035

Summary: A new method is provided for exact evaluation of the distribution of the amount of genetic material, from a chromosomal segment, shared identical-by-descent by a finite number of half-sibs. The interest in such distribution stems from its relation to the distribution of genetic material from chromosomal segments of an individual surviving to the next generation. The new method is superior to the existing one which has recently been suggested by *V. T. Stefanov* [J. Appl. Probab. 41, 345–354 (2004; Zbl 1053.62124)]. It allows both faster computation and a large number of half-sibs. Relevant software codes are provided for automated implementation of such evaluations.

MSC:

92D10	Genetics and epigenetics
60J20	Applications of Markov chains and discrete-time Markov processes on general state spaces (social mobility, learning theory, industrial processes, etc.)
92C40	Biochemistry, molecular biology

Cited in **2** Documents

Keywords:

identity-by-descent; continuous genome; genome survival; birth-death process; tables; irreducible continuous-time Markov chain

Full Text: DOI

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